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# 2024-25 Budget

ATGAGCCTGTGGCTGCCACGCGAGGCCACCGTGTAACCTGCCTCCCGTGCCCG  
TGAGCAAGGTGGTGAGCACCAGCAGTAGCTGGCCCGCAGCAACATCTACTA  
CCACGCCGGCAGCAGCGCCTGTGTGGCGTGCGGCCACCCCTATCTCCCACT  
AAGAAGCCCAACAACAACAAGATCTCTGGTGCCCAAGGTGAGCGGCTGCAG  
TACCGCGTGTTCGCACTCCACTGCCCGACGCCCAAGAAGTTCGGCTTCCCGA  
CACAAGCTTCTACAACCCCGACACCAGCCGCTGGTGGGCTGCGTGGGG  
GTGGAGTGGGGCGGCCAGCCCTGGGCGTGGGCATCAGCGGCCACCCCG  
TGCTGAACAAGCTGGACGACACCCGAGAACCGCCATCGCCCTACGCCCGCAACGC  
CGCGCTGGACAACCGCAGTGATCAGCATCAGCTACAGCAGCCAGCCAGCTG  
TGCTGTACGGCTGCAAGCCTCCCTACGCGCAGCACTGGGGCAAGGGCAGCC  
CCTGCACCAACGTGGCCGTGAACCCGGCGACTGCCCTCCGCTGGAGCTGAT  
CAACACCGTGATCAGGACGGCGACATGGTGAGCAACCGGCTTGGGCCCATG  
GACTTCACCAACCTTGACGGCCAACAAGAGCGAGGTGCCCTGGACATCTGCA  
CCAGCATCTGCAAGTACCCCGACTACATCAAGATGGTGAGCGAGCCCTACGG  
CGACAGCCTGTTCTTCTACTCTGCGCCGCGAGCAGATGTTGTGTCGCGCCACTGG  
TTAACCGCGCCGCGCGCTGGGGCAGAAGCTGCCCGACAGCTGTACATCAA  
GGCAGCGCGGACACCGCCAACCTGGCCAGCAGCAACTACTTCCCCACTCCC  
AGCGCGAGCATGTGTACCGCAGCGACGCCCAATCTTCAACAAGCCCTACCTGGC  
TGACGCGCGCCACGGGCCACAACAACCGCATCTGCTGGGGCAACCACTGTT  
CGTGACCGTGGTGGAACACACCCGACGACCAACATGAGCTGTGCGCCGCC  
ATCAGCACCGCAGCGAGACCTCAACAAGAACCAACTCAAGGAGTACCTG  
GCCACGGCAGGAGTACGACCTACGAGTTTCACTTCCAGCTGTGCAAGATCAC  
CTGACCGCGCAGCTGATGACCTACATCCACAGCATGAACAGACCATCTCTG  
GAGGACTGGAACCTTCGGCCTGCAGCCCCCTCCCGCGGTACACCTGGAGGACA  
CCTACCGCTTCGTGACCAACGCAAGCTATCGCTGCCCAGAACCCCTCC  
CGCTCCCAAGGAGGATTCCTCTGAAGAAATACACCTTCTGGGAGGTGAACCTG  
AAGGAGAAGTTACGCGCCGACCTGGACCAAGTTCCTCCCGTGGGCCGAAGTTC  
TGCTGACCGCCGCTGAAAGGCCAAGCCCAAGTTACCTTGGGCAAGCGCAA  
GGCCACCCCAACCCACGACGACACCAACCCGCCAAGCGCAAGGAAGCG  
CAAGCTGATAA

FIGURE 2

SEQ.ID.NO:2 Codon-Optimized HPV16 E1-G482D,W439R Mutant:

ATGCGCCGACCCCGCGCACCAACGGCGAGGAGGGCACCGGCTGCAACGGC  
TGGTTCTACGTGGAGGCCGTGGTGGAGAAGAAGACCGCGCAGCCATCAGCG  
ACGACGAGAACGAGAACGACAGCGACACCGCGCAGGACCTGGTGGACTTCA  
TCGTGAACGACAACGACTACCTGACCCAGGCCGAGACCGAGACCGCCACGC  
CCTGTTACCGCCAGGAGGCCAAGCAGCACCGCGCAGCCGTGACAGGTGCTG  
AAGCGCAAGTACCTGGGCGACCCCTGAGCGACATCAGCGGCTGCGTCGACA  
ACAACATCAGCCCCGCTGAAGGCCATCTGCATCGAGAAGCAGAGCCGCGC  
CGCAAGCGCCGCTGTTCGAGAGCGAGGACAGCGGCTACGGCAACACCGA  
GGTGGAGACCCAGCAGATGCTGCAGGTGGAGGGCGGCCACGAGACCGGAGC  
CCCCTGCAGCCAGTACAGCGGCGGCAGCGCGCGGCTGCAGCCAGTACAG  
AGCGGCAGCGGCGGCGAGGGCGTGAGCGAGCGCCACACCATCTGCCAGACC  
CCTCTGACCAACATCCTGAACGTGCTGAAGACCGCAACGCCAAGGCCGCCA  
TGCTGGCCAAAGTTCAAGGAGCTGTACGGCGTGAGCTTCAGCGAGCTGGTGGC  
CCCTTCAAGAGCAACAAGAGCACCTGCTGCGACTGGTGCATCGCCGCCCTTC  
GGCCTGACCCCCAGCATCGCCGACAGCATCAAGACCCCTGCTGCAGCAGTACT  
GCCTGTACCTGCACATCCAGAGCCTGGCCTGCAGCTGGGGCATGGTGGTGT  
GCTGCTGGTGCCTACAAGTGCGGCAAGAACC CGCAGACCATCGAGAAGCTG  
CTGAGCAAGCTGCTGTGCGTGAGCCCCATGTGCATGATGATCGAGCCTCCCA  
AGCTTCGAGCACCGCCGCCCTGTACTGGTACAAGACCGGCATCAGCAA  
CATCAGCGAGGTGTACGGCGCACACCCCGAGTGGATCCAGCGCCAGACCGTG  
CTGCAGCACAGCTTCAACGACTGCACCTTCGAGCTGAGCCAGATGGTGCAGT  
GGGCTACGACAACGACATCGTGGACGACAGCGAGATCGCCTACAAGTACGC  
CCAGCTGGCCGACACCAACAGCAACGCCAGCGCCTTCCTGAAGAGCAACAGC  
CAGGCCAAGATCGTGAAGGACTGCGCCACCATGTGCCGCCACTACAAGCGCG  
CCGAGAAGAAGCAGATGAGCATGAGCCAGTGGATCAAGTACCGCTGCGAGC  
CCGTGGACGACGGCGGCGACCGCAAGCAGATCGTGATGTTCTGCGCTACCA  
GGGCGTGGAATTATGAGCTTCCTGACCGCCCTGAAGCGCTTCCTGCAGGGC  
ATCCCAAGAAGAACTGCATCCTGCTGTACGGCGCCGCCAACACCGACAAGA  
GCCTGTTCCGCTAGAGCCTGATGAAGTTCCTGCAGGCGAGCGTGATCTGCTTC  
GTGAACAGCAAGAGCACTTCTGGCTGCAGCCCTGGCCGACGCCAAGATCG  
GCATGCTGGACGACGCCACCGTGCCCTGCTGGAACATACATCGACGACAACCT  
GCGCAACGCCCTGGACGGCAACCTGGTGAAGCATGGACGTGAAGCAGCCGCC  
CTGGTGCAGCTGAAGTGCCCTCCCTGCTGATCACCAGCAACATCAACGCCG  
GCACCGACAGCCGCTGGCCCTACCTGCACAACCGCCTGGTGGTGTTCACCTTC  
CCCAACGAGTTCCTTCGACGAGAAGCGTAACCCCGTGATACGAGCTGAACG  
ACAAGAACTGGAAGAGCTTCTTACGCCGACCTGGAGCGCGCCTGAGCCTGCA  
CGAGGACGAGGACAAGGAGAACGACGGCGCAGCCTGCCACCTTCAAGTG  
CGTAGCGGCCAGAACACCAACACCTGTAA

09642405.002100

103-104

ATGGAGACCCCTGTGCCAGCGCCTGAACGTGTGGCCAGGACAAGATCCTGACCC  
ACTACAGGAAAGACAGACAGCCAGCCTGTGCCGACCACCTGCACTACTGGAAGCA  
CATCGCGCTGGCCTTGCCTCTACTACTAACAGGCCGGAGATGGGCTTCAAG  
CACATCAACCACCAGGTGGTGCCCAACCCTGGCCGTGAGCAAGAACAAGGCC  
TGCAGGCCGCCGAGCTGCAGCTGACCTGACCTGGAGACCATCTACAACAGCCAGTA  
CAGCAACAGGAAGTGAGCCTGCAAGGACGTGAGCTGGAGGTGTACCTGACC  
GCCCCACC GGCTGCATCAAGAAGCAGCGGTACACCGTGGAGGTGCAGTTG  
ACGGCGACATCTGCAACACCATTGCACTACCAACATGAGCCACCATCTACAT  
TCTCGAGGAGGCCAGCGTGACCTGGTGGAGGGCAGGTTGGACTACTACGG  
CCTGTACTACTGCACAGAGGGCATCCGCACCTACTTCGTGCAGTTCAAGGAC  
GACGCCGAGAAGTACAGCAAGAAACAAGGTGTGGAGAGGTGCAGCCGCCGGC  
CAGGTGATCTCTGTGCCCAACGCGTGTTCAGCAGCAACGAGTTGAGCAGCC  
CCGAGGACATCCGCGAGCACTTGGCCAAACCAACAGCGCCGCCACCCACACCAA  
GGCGGTGGCCCTGGGCACCGAGGAGACCAAGACCATTCAGAGCGCCCGC  
AGCGAGCCCGACACCCGCAACCCCTGCCACACCAAGTGTCTGCACCGCG  
ACAGCGTGGACAGCGCCCATCTGACCGCCTTCAACAGCAGCCACAAGGG  
CCGCACTACCTGCAACAGCAACACCAACCCCATCTGTGACCTGAAGGGCGAC  
GCCAACACCTGGAAGTGCCTGCGCTACCGTTCAAGAAGCAAGCTGCAAGCTGT  
ACACCGCGTGAGCAGCACTTGGCACTGAGCAGGCCACAACGTGAAGACACA  
AGAGGCCCATCTGTGACCTGACCTACGACAGCGAGTGGCAGCGCGACCAAGTT  
CCTGAGCCAGGTGAAGATCCCCAAGACCATCACCGTGAGCACC GGCTTCATG  
AGCATCTAA

FIGURE 4

SEQ.ID.NO.:4 Codon-Optimized HPV16E7-C24G,E26G Mutant:

ATGCACGGCGACACCCCAACCCTGCACGAGTACATGCTGGACCTGCAGCCCG  
AGACCACCGACCTGTACGGCTACGGCCAGCTGAACGACAGCAGCGAGGAGG  
AGGACGAGATCGACGGCCCCGCCGGCCAGGCCGAGCCCGACCGCGCCCACT  
ACAACATCGTGACCTTCTGCTGCAAGTGCGACAGCACCCCTGCGCCTGTGCGT  
GCAGAGCACCCACGTGGACATCCGCACCCTGGAGGACCTGCTGATGGGCACC  
CTGGGCATCGTGTGCCCCATCTGCAGCCAGAAGCCCTAA

HPV16E7-C24G,E26G Mutant

FIGURE 5

SEQ.ID.NO.:5 Codon-Optimized HPV6a E7 Gene:

ATGCACGGCCGCCACGTGACCCCTGAAGGACATCGTGCTGGACCTGCAGCCTC  
CCGACCCCGTGGGCCTGCACTGCTACGAGCAGCTGGTGGACAGCAGCGAGGA  
CGAGGTGGACGAGGTGGACGGCCAGGACAGCCAGCCCTGAAGCAGCACTT  
CCAGATCGTGACCTGCTGCTGCGGCTGCGACAGCAACGTGCGCCTGGTGGTG  
CAGTGCACCGAGACCGACATCCGCGAGGTGCAGCAGCTCCTGCTGGGTACCC  
TGAACATCGTGTGCCCCATCTGCGCTCCCAAGACCTAA

002287-5042493

FIGURE 6

SEQ.ID.NO.:6 Codon-Optimized HPV18 E7 Gene:

ATGCACGGCCCCAAGGCCACCCTGCAGGACATCGTGCTGCACCTGGAGCCCC  
AGAACGAGATCCCCGTGGACCTGCTGTGCCACGAGCAGCTGAGCGACAGCGA  
GGAGGAGAACGACGAGATCGACGGCGTGAACACCAGCACCTGCCCCGCTCG  
CAGGGCCGAGCCCCAGCGCCACACCATGCTGTGCATGTGCTGCAAGTGCGAG  
GCCCCGATCGAGCTGGTGGTGGAGAGCAGCGCTGACGACCTGCGCGCCTTCC  
AGCAGCTGTTCTGAACACCCTGAGCTTCGTGTGCCCTGGTGCGCCAGCCAG  
CAGTAA

00642405-082100

FIGURE 7

SEQ.ID.NO.:7 Codon-Optimized HPV6a E2 Gene:

ATGGAGGCCATCGCCAAGCGCCTGGACGCCTGCCAGGAGCAGCTGCTGGAGC  
TGTACGAGGAGAAACAGCACCGACCTGCACAAGCACGTGCTGCACTGGAAGTG  
CATGCGCCACGAGAGCGTGCTGCTGTACAAGGCCAAGCAGATGGCCTGAGC  
CACATCGGCATGCAGGTGGTGCCTCCTCTGAAGGTGAGCGAGGCCAAGGGCC  
ACAACGCCATCGAGATGCAGATGCACCTCGAGAGCCTGCTGCGCACCGAGTA  
CAGCATGGAGCCCTGGACCCTGCAGGAGACCGACTACGAGATGTGGCAGACC  
CCTCCCAAGCGCTGCTTCAAGAAGCGCGGCAAGACCGTGGAGGTGAAGTTCG  
ACGGCTGCGCCAACAACACCATGGACTACGTGGTGTGGACCGACGTGTACGT  
GCAGGACAACGACACCTGGGTGAAGGTGCACAGCATGGTGGACGCCAAGGG  
CATCTACTACACCTGTGGCCAGTTCAAGACCTACTACGTGAACCTCGTGAAGG  
AGGCCGAGAAGTACGGCAGCACCAAGCACTGGGAGGTGTGCTACGGCAGCA  
CCGTGATCTGCAGCCCCGCTAGCGTGAGCAGCACCAACCCAGGAGGTGAGCAT  
CCCCGAGAGCACCACCTACACTCCCGCCCAGACCAGACCCCTGGTGAGCAGC  
AGCACCAAGGAGGACGCCGTGCAGACCCCTCCTCGCAAGCGCGCCCCGGC  
GTGCAGCAGAGCCCTGCAACGCCCTGTGCGTGGCCACATCGGCCCCGTGG  
ATAGCGGAACCACAACCTGATCACCAACAACCACGACCAGCACCAGCGCC  
GCAACAACAGCAACAGCAGCGCCACTCCCATCGTGCAGTTCCAGGGCGAGAG  
CAACTGCCTGAAGTGCTTCCGCTACCGCTGAACGATCGCAACCGCCACCTGT  
TCGACCTGATCAGCAGCACCTGGCACTGGGCCAGCAGCAAGGCTCCCCACAA  
GCACGCCATCGTGACCGTGACCTACGACAGCGAGGAGCAGCGCCAGCAGTTC  
CTGGACGTGGTGAAGATCCCTCCACCATCAGCCACAAGCTGGGCTTCATGA  
GCCTGCACCTGCTGTAA

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 217. **Figure 209**

ATGCAGACTCCCAAGGAGACCTTGAGCGAGCGCCTGAGCGCCCTGCAGGACA  
AGATCATCGACCATCAGGACAAGCAGACGAAGGACATCGACAGCCAGATCC  
AGTACTGGCAGCTGATCCGCTGGGAGAACGCCATCTTCTTGCCGGCTCGGA  
GCACGGGATCCAGACCCTGAACCACCAGGTGGTGCCCGCCTACAACATCAG  
AAGAGCAGGGCCCAACAGGCCATCGAGCTGCAGATGGCCCTGCAGGGCCCTG  
GCCAGAGCGCTCAAGAAGCCGAGGACTGGAACCTTGAGGACACCTGCGAG  
GAGCTGTGGAACACCGAGCCACCCACTGCTTCAAGAAGGGAGGCCAGACC  
GTGCAGGTGTACTTCGACGGCAACAAGGACAACATGTCATGAACATCGTGGCT  
GGGACAGCTGTACTACATGACCAAGCCGCGCACTGGGACAGACGCCCTC  
CTGGCTGAGCCACCGCGGGCTGTACTACGTGAAGAGGGCTACAAACCTTC  
TACATCGAGTTCAAGAGCGAGTCGGAGAGAAGTACGGCAACACCGGCCACTGG  
GAGGTGCATCTCGGCAACAACGTGATCGACTGCAACGACAGCATGTGCAGCA  
CAGCGACGACACCGGTAGCGCCACCCAGCTGGTGAAGAGAGCTCGAGCACAC  
TCCAGCCCTCACAGCAGCACCGTGAAGCTGGGCACCCGCCAAGACATCGGC  
CAGACCAAGCCGCCCATCGCCTGGCCCTGCGGCTGGCCGAGAACAGCAGC  
ACTCGGGGCCCGTGAACCTCTGCTGGCGCGGCCACCGCCACCGGCAACAA  
CAAGCGCCGCAAGCTGTGACAGCGGCAACACCATTCCCATCATCCACTGAAG  
GGCGACCCGCAAGCCTGAAGTGCTTGCCTACCGCGCTGCGCAAGCAGCAGG  
ACCATTACCGCGACATCAGACGACCTGGCACTGGACGGCGCGCCGGGAACGA  
GAAGACCGGCATCTGACCGTGACCTACCAAGCGAGACCCAGCGACCAAG  
TTCTGAACACCGTGGCCATCCCCGACAGCGTGCAGATCTGTGGGTGCTACA  
TGACCATGTAA

001280-50124960

FIGURE 9.  
Comparison of protein expression of  
native and synthetic HPV16 L1 genes

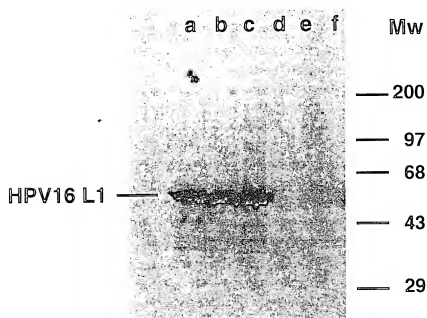


FIGURE 10

Comparison of protein expression  
of native and synthetic HPV 16 E1 genes

a b c d e

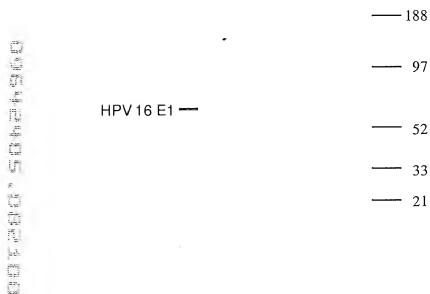
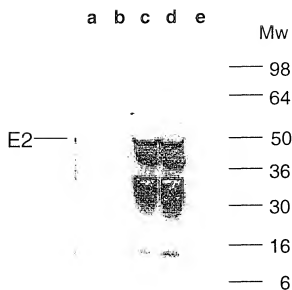


FIGURE 11.

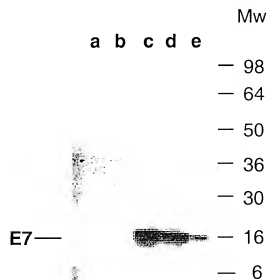


a. mock  
b. lacZ  
c. synthetic 16 E2 isolate 6  
d. synthetic 16 E2 isolate 11  
e. native 16 E2

xmw98.75 16557-27

FIGURE 12

Comparison of protein expression of  
native and synthetic HPV16 E7 genes



a. mock

b. lacZ

c. synthetic HPV16 E7 isolate 2

d. synthetic HPV16 E7 isolate 4

e. native HPV16 E7

xmw98.75 16557-27

FIGURE 13

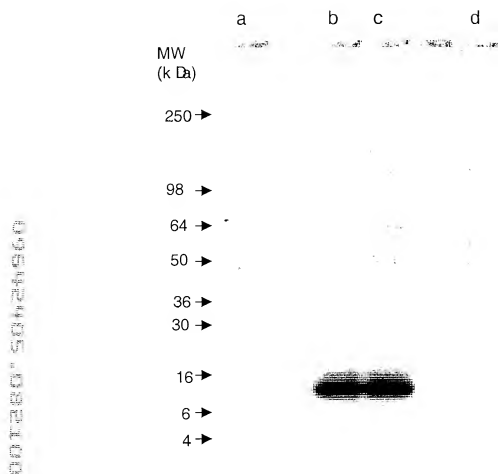
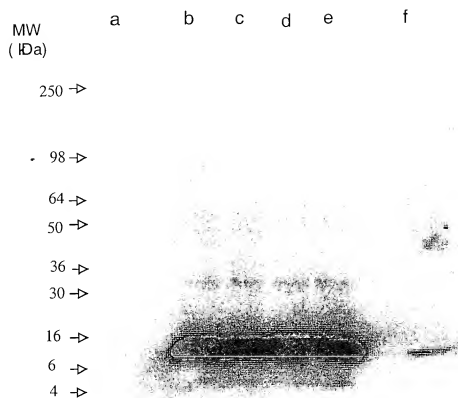


FIGURE 14



001230-50121960

## Expression of synthetic HPV 6 E2 gene

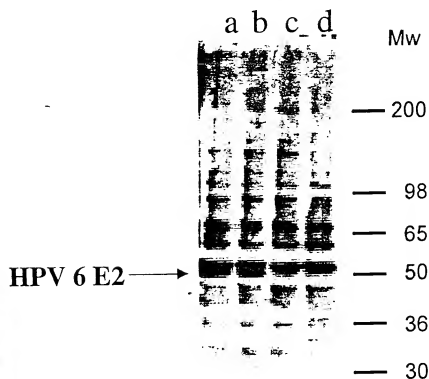


Figure 15. Expression of a synthetic gene encoding HPV 6 E2 protein. 293 cells were transfected with synthetic HPV 6 E2 or control plasmids or were mock transfected. Cell lysates were prepared 48 hr. later, fractionated by SDS PAGE and analyzed by immunoblotting using a goat anti-6E2 antiserum as first antibody. a. 6 E2-5.4; b. 6E2-5.5; c. beta-gal; d. mock.



# Expression of synthetic HPV 18 E2 gene

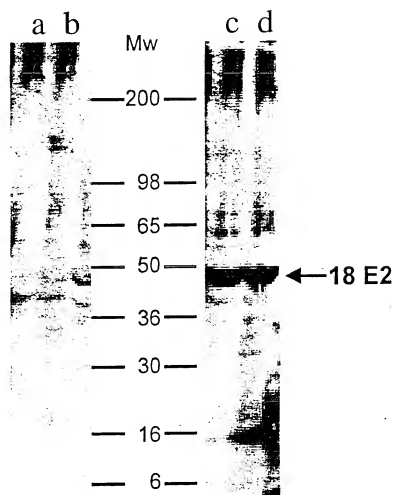


Figure 16. Expression of a synthetic gene encoding HPV 18 E2 protein. 293 cells were transfected with synthetic HPV 18 E2 or control plasmids or were mock transfected. Cell lysates were prepared 48 hr. later, fractionated by SDS PAGE and analyzed by immunoblotting using a goat anti- 18E2 antiserum as first antibody. a. beta-gal; b. mock; c. 18 E2-4.4; d. 18E2-4.5.

FIGURE 17

HPV16 L1 Gene-Building Oligomers

MN4A1 (SEQ.ID.NO:9) 5' ATG AGC CTG TGG CTG CCC AGC GAG GCC ACC  
GTG TAC CTG CCT CCC GTG CCC GTG AGC AAG GTG GTG AGC ACC GAC  
GAG TAC GTG GCC CGC ACC AAC ATC TAC TAC CAC GCC GGC ACC AGC  
CGC CTG CTG 3'

MN4A3 (SEQ.ID.NO:10) 5' CGC ATC CAC CTG CCC GAC CCC AAC AAG TTC  
GGC TTC CCC GAC ACA AGC TTC TAC AAC CCC GAC ACC CAG CGC CTG  
GTG TGG GCC TGC GTG GGC GTG GAG GTG GGC CGC GGC CAG CCC CTG  
GGC GTG GGC 3'

MN4A5 (SEQ.ID.NO:11) 5' GAG TGC ATC AGC ATG GAC TAC AAG CAG ACC  
CAG CTG TGC CTG ATC GGC TGC AAG CCT CCC ATC GGC GAG CAC TGG  
GGC AAG GGC AGC CCC TGC ACC AAC GTG GCC GTG AAC CCC GGC GAC  
TGC CCT CCC 3'

MN4A7 (SEQ.ID.NO:12) 5' GCC AAC AAG AGC GAG GTG CCC CTG GAC ATC  
TGC ACC AGC ATC TGC AAG TAC CCC GAC TAC ATC AAG ATG GTG AGC  
GAG CCC TAC GGC GAC AGC CTG TTC TTC TAC CTG CGC CGC GAG CAG  
ATG TTC GTG CGC 3'

MN4A9 (SEQ.ID.NO:13) 5' GCC AGC AGC AAC TAC TTC CCC ACT CCC AGC  
GGC AGC ATG GTG ACC AGC GAC GCC CAA ATC TTC AAC AAG CCC TAC  
TGG CTG CAG CGC GCC CAG GGC CAC AAC AAC GGC ATC TGC TGG GGC  
AAC CAG CTG 3'

MN4A11 (SEQ.ID.NO:14) 5' GAG TAC CTG CGC CAC GGC GAG GAG TAC GAC  
CTG CAG TTC ATC TTC CAG CTG TGC AAG ATC ACC CTG ACC GCC GAC  
GTG ATG ACC TAC ATC CAC AGC ATG AAC AGC ACC ATC CTG GAG GAC  
TGG AAC TTC GGC CTG 3'

MN4A13 (SEQ.ID.NO:15) 5' GCT CCC AAG GAG GAT CCC CTG AAG AAG TAC  
ACC TTC TGG GAG GTG AAC CTG AAG GAG AAG TTC AGC GCC GAC CTG  
GAC CAG TTC CCC CTG GGC CGC AAG TTC CTG CTG CAG GCC GGC CTG  
AAG GCC AAG CCC AAG 3'

MN4A2 (SEQ.ID.NO:16) 5' GTT GGG GTC GGG CAG GTG GAT GCG GAA CAC  
CGG GTA CTG CAG GCC GCT CAC CTT GGG CAC CAG GAT CTT GTT GTT  
GTT GGG CTT CTT GAT GGG GAA GTA GGG GTG GCC CAC GGC CAG CAG  
CGG GCT GGT GCC GGC 3'

[illegible][illegible][illegible][illegible][illegible][illegible][illegible][illegible]

**Figure 1.** The effect of the number of trials on the mean accuracy of the responses ( $n = 10$ ) as a function of the number of items presented at once. The error bars represent the standard error of the mean.

[illegible][illegible][illegible]



FIGURE 18

**HPV16E1 Gene-building Oligomers**

MN605 (SEQ.ID.NO:33) 5' ATG GCC GAC CCC GCC GGC ACC AAC GGC GAG  
GAG GGC ACC GGC TGC AAC GGC TGG TTC TAC GTG GAG GCC GTG GTG  
GAG AAG AAG ACC GGC GAC GCC ATC AGC GAC GAC GAG AAC GAG AAC  
GAC AGC GAC 3'

MN606 (SEQ.ID.NO:34) 5' GTG CTG CTT GGC CTC CTG GGC GGT GAA CAG  
GGC GTG GGC GGT CTC GGT CTC GGC CTG GGT CAG GTA GTC GTT GTC  
GTT CAC GAT GAA GTC CAC CAG GTC CTC GCC GGT GTC GCT GTC GTT  
CTC GTT CTC GTC 3'

MN607 (SEQ.ID.NO:35) 5' GCC CAG GAG GCC AAG CAG CAC CGC GAC GCC  
GTG CAG GTG CTG AAG CGC AAG TAC CTG GGC AGC CCC CTG AGC GAC  
ATC AGC GGC TGC CTC GAC AAC AAC ATC AGC CCC CGC CTG AAG GCC  
ATC TGC ATC GAG 3'

MN608 (SEQ.ID.NO:36) 5' CTC GTG GCG GCC CTC CAC CTG CAG CAT CTG  
CTG GGT CTC CAC CTC GGT GTT GCC GTA GCC GCT GTC CTC GCT CTC GAA  
CAG GCG GCG CTT GGC GGC GCG GCT CTG CTT CTC GAT GCA GAT GGC  
CTT CAG GC 3'

MN609 (SEQ.ID.NO:37) 5' CAG GTG GAG GGC CGC CAC GAG ACC GAG ACC  
CCC TGC AGC CAG TAC AGC GGC GGC AGC GGC GGC GGC TGC AGC CAG  
TAC AGC AGC GGC AGC GGC GGC GAG GGC GTG AGC GAG CGC CAC ACC  
ATC TGC CAG ACC 3'

MN610 (SEQ.ID.NO:38) 5' CTT GAA GGG GCG CAC CAG CTC GCT GAA GCT  
CAC GCC GTA CAG CTC CTT GAA CTT GGC CAG CAT GGC GGC CTT GGC  
GTT GCT GGT CTT CAG CAC GTT CAG GAT GTT GGT CAG AGG GGT CTG  
GCA GAT GGT GTG GCG 3'

MN611 (SEQ.ID.NO:39) 5' GAG CTG GTG CGC CCC TTC AAG AGC AAC AAG  
AGC ACC TGC TGC GAC TGG TGC ATC GCC GCC TTC GGC CTG ACC CCC  
AGC ATC GCC GAC AGC ATC AAG ACC CTG CTG CAG CAG TAC TGC CTG  
TAC CTG CAC ATC CAG 3'

MN612 (SEQ.ID.NO:40) 5' CAT GGG GCT CAC GCA CAG CAG CTT GCT CAG  
CAG CTT CTC GAT GGT CTC GCG GTT CTT GCC GCA CTT GTA GCG CAC  
CAG CAG CAG CAC CAC CAT GCC CCA GCT GCA GGC CAG GCT CTG GAT  
GTG CAG GTA CAG GCA G 3'

004445-102490

**Abstract**

MN614 (SEQ.ID.NO:42) 5' GGC GAT CTC GCT GTC GTC CAC GAT GTC GTT  
 GTC GTA GGC CCA CTG CAC CAT CTG GCT CAG CTC GAA GGT GCA GTC  
 GTT GAA GCT GTG CTG CAG CAC GGT CTG GCG CTG GAT CCA CTC GGG  
 GGT GAT GCC 3'

MN615 (SEQ.ID.NO:43): 5' GTG GAC GAC AGC GAG ATC GCC TAC AAG TAC  
 GCC CAG CTG GCC GAC ACC AAC AGC AAC GCC AGC GCC TTC CTG AAG  
 AGC AAC AGC CAA GGC CAA GAT CGT GAA GGA CTG CGC CAC CAT GTG  
 CCG CCA CTA C 3'

MN616 (SEQ.ID.NO:44) 5' GTA GCG CAG GAA CAT CAC GAT CTG CTT GCG  
 GTC GCC GCC GTC GTC CAC GCG GTC GCA GCG GTA CTT GAT CCA CTG  
 GCT CAT GCT CAT CTG CTT CTT CTC GGC GCG CTT GTA GTG GCG GCA CAT  
 GGT GGC 3'

MN617 (SEQ.ID.NO:45) 5' CAG ATC GTG ATG TTC CTG CGC TAC CAG GGC  
GTG GAA TTC ATG AGC TTC CTG ACC GCC CTG AAG CGC TTC CTG CAG  
GGC ATC CCC AAG AAG AAC TGC ATC CTG CTG TAC GGC GCC GCC AAC  
ACC GAC AAG 3'

MN618 (SEQ.ID.NO:46) 5' GCC GAT CTT GGC GTC GGC CAG GGG CTG CAG  
CCA GAA GTG GCT CTT GCT GTT CAC GAA GCA GAT CAC GCT GCC CTG  
CAG GAA CTT CAT CAG GCT CAT GCC GAA CAG GCT CTT GTC GGT GTT  
GGC GGC GCCG 3'

MN619 (SEQ.ID.NO:47) 5' CTG GCC GAC GCC AAG ATC GGC ATG CTG GAC  
GAC GCC ACC GTG CCC TGC TGG AAC TAC ATC GAC GAC AAC CTG CGC  
AAC GCC CTG GAC GGC AAC CTG GTG AGC ATG GAC GTG AAG CAC CGC  
CCC CTG GTG 3'

MN620 (SEQ.ID.NO:48) 5' GAA CTC GTT GGG GAA GGT GAA CAC CAC CAG  
GCG GTT GTG CAG GTA GGG CCA GCG GCT GTC GGT GCC GGC GTT GAT  
GTT GCT GGT GAT CAG CAG GGG AGG GCA CTT CAG CTG CAC CAG GGG  
GCG GTG CAC CAG 3'



FIGURE 19

**Oligonucleotides used in the generation of synthetic HPV 16 E2**

13856-307-2A (SEQ.ID.NO:65) 5' ATG GAG ACC CTG TGC CAG CGC CTG AAC  
GTG TGC CAG GAC AAG ATC CTG ACC CAC TAC GAG AAC GAC AGC ACC  
GAC CTG CGC GAC CAC ATC GAC TAC TGG 3'

13856-307-2C (SEQ.ID.NO:66) 5' CCA CCA GGT GGT GCC CAC CCT GGC CGT  
GAG CAA GAA CAA GGC CCT GCA GGC CGC CGA GCT GCA GCT GAC CCT  
GGA GAC GAT CTA CAA CAG CCA GTA CAG CAA CG 3'

13856-307-2E (SEQ.ID.NO:67) 5' CCG GCT GCA TCA AGA AGC ACG GCT ACA  
CCG TGG AGG TGC AGT TCG ACG GCG ACA TCT GCA ACA CCA TGC ACT  
ACA CCA ACT GGA CCC ACA TTT ACA TCT GTG AGG AGG 3'

13856-307-2G (SEQ.ID.NO:68) 5' CGT GCA CGA GGG GAT CCG CAC CTA CTT  
CGT GCA GTT CAA GGA CGA CGC CGA GAA GTA CAG CAA GAA CAA GGT  
GTG GGA GGT GCA CGC CGG AGG CCA GGT GAT CC 3'

13856-307-2I (SEQ.ID.NO:69) 5' GGC CAA CCA CAG CGC CGC CAC CCA CAC  
CAA GGC CGT GGC CCT GGG CAC CGA GGA GAC CCA GAC CAC AAT CCA  
GCG CCC TCG CAG CGA GCC CGA CAC CGG CAA CCC CTG CC 3'

13856-307-2K (SEQ.ID.NO:70) 5' GCC ACA AGG GCC GGA TCA ACT GCA ACA  
GCA ACA CCA CCC CTA TCG TGC ACC TGA AGG GCG ACG CCA ACA CCC  
TGA AGT GCC TGC GGT ACC GCT TCA AGA AGC ACT GC 3'

13856-307-2B (SEQ.ID.NO:71) 5' CCA GGG TGG GCA CCA CCT GGT GGT TGA  
TGT GCT TGA AGC CCA TCT CGC GGG CCT TGT AGT AGA TGG CGC AGG  
CCA GGC GCA TGT GCT TCC AGT AGT CGA TGT GGT CGC GCA GG 3'

13856-307-2D (SEQ.ID.NO:72) 5' GCC GTG CTT CTT GAT GCA GCC GGT AGG  
GGC GGT GAG GTA CAC CTC CAG GCT CAC CTC CTG CAG GGT CCA CTT  
CTC GTT GCT GTA CTG GCT GTT GTA GAT CG 3'

13856-307-2F (SEQ.ID.NO:73) 5' GGT GCG GAT CCC CTC GTG CAC GTA GTA  
CAG GCC GTA GTA GTC CAC CTG GCC CTC CAC CAC GGT CAC GCT GGC  
CTC CTC ACA GAT GTA AAT GTG GGT CC 3'

13856-307-2H (SEQ.ID.NO:74) 5' GGG TGG CGG CGC TGT GGT TGG CCA GGT  
GCT GGC GGA TCG TCT CGG GGC TGC TCA CCT CGT TGC TGC TGA ACA  
CGC TGG TGG GGC ACA GGA TCA CCT GGC CTC CGG CGT GC 3'

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FIGURE 19, CTD. 2/2

13856-307-2J (SEQ.ID.NO:75) 5' GCA GTT GAT CCG GCC CTT GTG GCT GCT  
GTT GAA GGC GGT CAG GAT AGG GGC GCT GTC GAC GCT GTC GCG GTG  
CAG CAG CTT GGT GGT GTG GCA GGG GTT GCC GGT GTC GGG 3'

13856-307-2L (SEQ.ID.NO:76) 5' CGT AGG TCA GGG TCA CGA TAG CGC TCT  
TGT GCT TCA CGT TGT GGC CGG TCC AGT GCC AGG TGC TGC TCA CGG  
CGG TGT ACA GCT TGC AGT GCT TCT TGA AGC GGT ACC GC 3'

13856-307-2M (SEQ.ID.NO:77) 5' TTT AGA TGC TCA TGA AGC CGG TGC TCA  
CGG TGA TGG TCT TGG GGA TCT TCA CCT GGC TCA GGA ACT GGT CGC  
GCT GCC ACT CGC TGT CGT AGG TCA GGG TCA CGA TAG CGC 3'

13856-307-2PA (SEQ.ID.NO:78) 5' CGA GCT GAT ATC GAA TTC AGA TCT GCC  
ACC ATG GAG ACC CTG TGC CAG CG 3'

13856-307-2PM (SEQ.ID.NO:79) 5' GGT TGC AGA TCT AGA CTC GAG TTT AGA  
TGC TCA TGA AGC CGG TGC 3'

13856-307-2PE (SEQ.ID.NO:80) 5' CCG GCT GCA TCA AGA AGC ACG 3'

13856-307-2PI (SEQ.ID.NO:81) 5' GGC CAA CCA CAG CGC CGC C 3'

13856-307-2PD (SEQ.ID.NO:82) 5' GCC GTG CTT CTT GAT GCA GCC 3'

13856-307-2PH (SEQ.ID.NO:83) 5' GGG TGG CGG CGC TGT GG 3'

13856-307-2PL (SEQ.ID.NO:84) 5' CGT AGG TCA GGG TCA CGA TAG C 3'

13856-307-2J  
13856-307-2L  
13856-307-2M  
13856-307-2PA  
13856-307-2PM  
13856-307-2PE  
13856-307-2PI  
13856-307-2PD  
13856-307-2PH  
13856-307-2PL

FIGURE 20

**Oligonucleotides used in the generation of synthetic HPV 16 E7.**

13856-307-7A (SEQ.ID.NO:85) 5' GGC CGG AGA TCT GAT ATC GAA TTC GCC  
ACC ATG CAC GGC GAC ACC CCC ACC CTG CAC GAG TAC ATG CTG GAC  
CTG CAG CCC GAG ACC ACC GAC CTG TAC GGC TAC GGC C 3'

13856-307-7C (SEQ.ID.NO:86) 5' GCC GAG CCC GAC CGC GCC CAC TAC AAC  
ATC GTG ACC TTC TGC TGC AAG TGC GAC AGC ACC CTG CGC CTG TGC  
GTG CAG AGC ACC CAC GTC GAC ATC CGC ACC CTG G 3'

13856-307-7B (SEQ.ID.NO:87) 5' GGG CGC GGT CGG GCT CGG CCT GGC CGG  
CGG GGC CGT CGA TCT CGT CCT CTT CCT CGC TGC TGT CGT TCA GCT GGC  
CGT AGC CGT ACA GGT CGG TGG 3'

13856-307-7D (SEQ.ID.NO:88) 5' CCG CGG CAG ATC TAG ACT CGA GTT TAG  
GGC TTC TGG CTG CAG ATT GGG CAC ACG ATT CCC AGG GTG CCC ATC  
AGC AGG TCC TCC AGG GTG CGG ATG TCG ACG TGG G 3'

13856-307-7PA (SEQ.ID.NO:89) 5' GGC CGG AGA TCT GAT ATC GAA TTC G 3'

13856-307-7PD (SEQ.ID.NO:90) 5' CCG CGG CAG ATC TAG ACT CG 3'

001230-5042960

FIGURE 21

**Oligonucleotides Used for Construction of HPV6a E7 Gene**

**A. DNA Template Oligos**

LS207 (105-mer) (SEQ.ID.NO:91) 5' GTC ACA GAT CTG ATA TCG AAT TCC ACC  
ATG CAC GGC CGC CAC GTG ACC CTG AAG GAC ATC GTG CTG GAC CTG  
CAG CCT CCC GAC CCC GTG GGC CTG CAC TGC TAC 3'

LS208 (105-mer) (SEQ.ID.NO:92) 5' CTG GAA GTG CTG CTT CAG GGG CTG GCT  
GTC CTG GCC GTC CAC CTC GTC CAC CTC GTC CTC GCT GCT GTC CAC CAG  
CTG CTC GTA GCA GTG CAG GCC CAC GGG GTC 3'

LS209 (107-mer) (SEQ.ID.NO:93) 5' CCA GCC CCT GAA GCA GCA CTT CCA GAT  
CGT GAC CTG CTG CTG CGG CTG CGA CAG CAA CGT GCG CCT GGT GGT  
GCA GTG CAC CGA GAC CGA CAT CCG CGA GGT GCA GC 3'

LS210 (102-mer) (SEQ.ID.NO:94) 5' CAG TCA GAT CTA GAG ATA TCT TTA GGT  
CTT GGG AGC GCA GAT GGG GCA CAC GAT GTT CAG GGT ACC CAG CAG  
GAG CTG CTG CAC CTC GCG GAT GTC GGT CTC 3'

**B. PCR Amplification Primers**

LS211 (24-mer) (SEQ.ID.NO:95) 5' GTC ACA GAT CTG ATA TCG AAT TCC 3'

LS212 (26-mer) (SEQ.ID.NO:96) 5' CAG TCA GAT CTA GAG ATA TCT TTA GG 3'

FIGURE 22

**Oligonucleotides Used for Construction of HPV18 E7 Gene**

A. DNA Template Oligos

LS201 (109-mer) (SEQ.ID.NO:97) 5' GTC ACA GAT CTG ATA TCG AAT TCC ACC  
ATG CAC GGC CCC AAG GCC ACC CTG CAG GAC ATC GTG CTG CAG CTG  
GAG CCC CAG AAC GAG ATC CCC GTG GAC CTG CTG TGC C 3'

LS202 (111-mer) (SEQ.ID.NO:98) 5' GGG CTC GGC CCT GCG AGC GGG CAG  
GTG CTG GTG GTT CAC GCC GTC GAT CTC GTC GTT CTC CTC GCT GTC  
GCT CAG CTG CTC GTG GCA CAG CAG GTC CAC GGG GAT CTC 3'

LS203 (108-mer) (SEQ.ID.NO:99) 5' GCC CGC TCG CAG GGC CGA GCC CCA  
GCG CCA CAC CAT GCT GTG CAT GTG CTG CAA GTG CGA GGC CCG CAT  
CGA GCT GGT GGT GGA GAG CAG CGC TGA CGA CCT GCG CGC 3'

LS204 (109-mer) (SEQ.ID.NO:100) 5' CAG TCA GAT CTA GAG ATA TCT TTA  
CTG CTG GCT GGC GCA CCA GGG GCA CAC GAA GCT CAG GGT GTT CAG  
GAA CAG CTG CTG GAA GGC GCG CAG GTC GTC AGC GCT GCT C 3'

B. PCR Amplification Primers

LS205 (26-mer) (SEQ.ID.NO:101) 5' GTC ACA GAT CTG ATA TCG AAT TCC AC  
3'

LS206 (27-mer) (SEQ.ID.NO:102) 5' CAG TCA GAT CTA GAG ATA TCT TTA CTG  
3'

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FIGURE 23

Oligonucleotides used in the construction of HPV6 E2

6A 1-84 (90mer) (SEQ.ID.NO:103) 5' GAA TTC AGA TCT GAT ATC ACC ATG  
GAG GCC ATC GCC AAG CGC CTG GAC GCC TGC CAG GAG CAG CTG CTG  
GAG CTG TAC GAG GAG AAC AGC 3'

6B 65-157 (92mer) (SEQ.ID.NO:104) 5' CCT TGT ACA GCA GCA CGC TCT  
CGT GGC GCA TGC ACT TCC AGT GCA GCA CGT GCT TGT GCA GGT CGG  
TGC TGT TCT CCT CGT ACA GCT CCA GC 3'

6C 132-227 (96mer) (SEQ.ID.NO:105) 5' CCA CGA GAG CGT GCT GCT GTA  
CAA GGC CAA GCA GAT GGG CCT GAG CCA CAT CGG CAT GCA GGT GGT  
GCC TCC TCT GAA-GGT GAG CGA GGC CAA GGG 3'

6D 202-304 (103mer) (SEQ.ID.NO:106) 5' GCA GGG TCC AGG GCT CCA TGC  
TGT ACT CGG TGC GCA GCA GGC TCT CGA GGT GCA TCT GCA TCT CGA  
TGG CGT TGT GGC CCT TGG CCT CGC TCA CCT TCA GAG G 3'

6E 276-373 (98mer) (SEQ.ID.NO:107) 5' CGA GTA CAG CAT GGA GCC CTG  
GAC CCT GCA GGA GAC CAG CTA CGA GAT GTG GCA GAC CCC TCC CAA  
GCG CTG CTT CAA GAA GCG CGG CAA GAC CGT GG 3'

6F 347-448 (102mer) (SEQ.ID.NO:108) 5' CGT TGT CCT GCA CGT ACA CGT  
CGG TCC ACA CCA CGT AGT CCA TGG TGT TGT TGG CGC AGC CGT CGA  
ACT TCA CCT CCA CGG TCT TGC CGC GCT TCT TGA AGC 3'

6G 425-526 (102mer) (SEQ.ID.NO:109) 5' CCG ACG TGT ACG TGC AGG ACA  
ACG ACA CCT GGG TGA AGG TGC ACA GCA TGG TGG ACG CCA AGG GCA  
TCT ACT ACA CCT GTG GCC AGT TCA AGA CCT ACT ACG 3'

6H 495-586 (92mer) (SEQ.ID.NO:110) 5' GCT GCC GTA GCA CAC CTC CCA  
GTG CTT GGT GCT GCC GTA CTT CTC GGC CTC CTT CAC GAA GTT CAC GTA  
GTA GGT CTT GAA CTG GCC ACA GG 3'

6I 500-591 (94mer) (SEQ.ID.NO:111) 5' GCA CTG GGA GGT GTG CTA CGG  
CAG CAC CGT GAT CTG CAG CCC CGC TAG CGT GAG CAG CAC CAC CCA  
GGA GGT GAG CAT CCC CGA GAG CAC CAC C 3'

6J 636-732 (97mer) (SEQ.ID.NO:112) 5' GCG AGG AGG GGT CTG CAC GGC  
GTC CTC CTT GGT GCT GCT GCT CAC CAG GGT GCT GGT CTG GGC GGG  
AGT GTA GGT GGT GCT CTC GGG GAT GCT CAC C 3'

0054106-08100

FIGURE 23, CTD. 2/2

6K 708-804 (97mer) (SEQ.ID.NO:113) 5' GGA CGC CGT GCA GAC CCC TCC  
TCG CAA GCG CGC CCG CGG CGT GCA GCA GAG CCC CTG CAA CGC CCT  
GTG CGT GGC CCA CAT CGG CCC CGT GGA CAG C 3'

6L 780-873 (94mer) (SEQ.ID.NO:114) 5' GGC GCT GCT GTT GCT GTT GTT  
GCG GCG CTG GTG CTG GTC GTG GTT GTT GGT GAT CAG GTT GTG GTT  
GCC GCT GTC CAC GGG GCC GAT GTG GGC C 3'

6M 849-943 (95mer) (SEQ.ID.NO:115) 5' CCG CAA CAA CAG CAA CAG CAG  
CGC CAC TCC CAT CGT GCA GTT CCA GGG CGA GAG CAA CTG CCT GAA  
GTG CTT CCG CTA CCG CCT GAA CGA TCG CC 3'

6N 917-1012 (96mer) (SEQ.ID.NO:116) 5' CGT GCT TGT GGG GAG CCT TGC  
TGC TGG CCC AGT GCC AGG TGC TGC TGA TCA GGT CGA ACA GGT GGC  
GGT GGC GAT CGT TCA GGC GGT AGC GGA AGC 3'

6O 989-1083 (95mer) (SEQ.ID.NO:117) 5' GCA GCA AGG CTC CCC ACA AGC  
ACG CCA TCG TGA CCG TGA CCT ACG ACA GCG AGG AGC AGC GCC AGC  
AGT TCC TGG ACG TGG TGA AGA TCC CTC CC 3'

6P 1059-1154 (96mer) (SEQ.ID.NO:118) 5' CTC GAG AGA TCT CCC GGG TCT  
AGA GCT TAC AGC AGG TGC AGG CTC ATG AAG CCC AGC TTG TGG CTG  
ATG GTG GGA GGG ATC TTC ACC ACG TCC AGG 3'

6PA 25mer (SEQ.ID.NO:119) 5' GAA TTC AGA TCT GAT ATC ACC ATG G 3'

6PD 21mer (SEQ.ID.NO:120) 5' GCA GGG TCC AGG GCT CCA TGC 3'

6PE 25mer (SEQ.ID.NO:121) 5' CGA GTA CAG CAT GGA GCC CTG GAC C 3'

6PH 25mer (SEQ.ID.NO:122) 5' GCT GCC GTA GCA CAC CTC CCA GTG C 3'

6PI 21mer (SEQ.ID.NO:123) 5' GCA CTG GGA GGT GTG CTA CGG 3'

6PL 23mer (SEQ.ID.NO:124) 5' GGC GCT GCT GTT GCT GTT GTT GC 3'

6PM 22mer (SEQ.ID.NO:125) 5' CCG CAA CAA CAG CAA CAG CAG C 3'

6PP 26mer (SEQ.ID.NO:126) 5' CTC GAG AGA TCT CCC GGG TCT AGA GC 3'

0064405-082100

FIGURE 24

Oligonucleotides used to construct HPV18 E2

18A 1-97 (97mer) (SEQ.ID.NO:127) 5'GAA TTC AGA TCT GAT ATC ACC ATG  
CAG ACT CCC AAG GAG ACC CTG AGC GAG CGC CTG AGC GCC CTG CAG  
GA CAA GAT CAT CGA CCA CTA CGA GAA CG 3'

18B 69-166 (98mer) (SEQ.ID.NO:128) 5'CGA AGA AGA TGG CGT TCT CCC  
AGC GGA TCA GCT GCC AGT ACT GGA TCT GGC TGT CGA TGT CCT TGC  
TGT CGT TCT CGT AGT GGT CGA TGA TCT TGT CC 3'

18C 141-234 (94mer) (SEQ.ID.NO:129) 5'CCG CTG GGA GAA CGC CAT CTT  
CTT CGC CGC TCG CGA GCA CGG GAT CCA GAC CCT GAA CCA CCA GGT  
GGT GCC CGC CTA CAA CAT CAG CAA GAG C 3'

18D 211-304 (94mer) (SEQ.ID.NO:130) 5'CCT CGG TCT TGT AGG CGC TCT  
GGG CCA GGC CCT GCA GGG CCA TCT GCA GCT CGA TGG CCT TGT GGG  
CCT TGC TCT TGC TGA TGT TGT AGG CGG G 3'

18E 281-371 (91mer) (SEQ.ID.NO:131) 5'CCC AGA GCG CCT ACA AGA CCG  
AGG ACT GGA CCC TGC AGG ACA CCT GCG AGG AGC TGT GGA ACA CCG  
AGC CCA CCC ACT GCT TCA AGA AGG G 3'

18F 348-441 (94mer) (SEQ.ID.NO:132) 5'GCT GTC CCA GGC CAC GTA GTT  
CAT GCA GTT GTC CTT GTT GCC GTC GAA GTA CAC CTG CAC GGT CTG  
GCC TCC CTT CTT GAA GCA GTG GGT GGG C 3'

18G 416-505 (90mer) (SEQ.ID.NO:133) 5'GCA TGA ACT ACG TGG CCT GGG  
ACA GCG TGT ACT ACA TGA CCG ACG CCG GCA CCT GGG ACA AGA CCG  
CCA CCT GCG TGA GCC ACC GCG GCC 3'

18H 481-572 (92mer) (SEQ.ID.NO:134) 5'CCG TAC TTC TCG CAC TCG CTC  
TTG AAC TCG ATG TAG AAG GTG TTG TAG CCC TCC TTC ACG TAG TAC  
AGG CCG CGG TGG CTC ACG CAG GTG GC 3'

18I 543-636 (94mer) (SEQ.ID.NO:135) 5'CGA GTT CAA GAG CGA GTG CGA  
GAA GTA CGG CAA CAC CGG CAC CTG GGA GGT GCA CTT CGG CAA CAA  
CGT GAT CGA CTG CAA CGA CAG CAT GTG C 3'

18J 609-708 (100mer) (SEQ.ID.NO:136) 5'GCT GTA GGG GCT GGG AGT GTG  
CTG CAG CTG CTT CAC CAG CTG GGT GGC GCT CAC GGT GTC GTC GCT  
GGT GCT GCA CAT GCT GTC GTT GCA GTC GAT CAC G 3'

001250-5042163

FIGURE 24, CTD. 2/2

18K 687-779 (93mer) (SEQ.ID.NO:137) 5' GCA CAC TCC CAG CCC CTA CAG  
CAG CAC CGT GAG CGT GGG CAC CGC CAA GAC CTA CGG CCA GAC CAG  
CGC CGC CAC TCG CCC TGG CCA CTG CGG 3'

18L 758-853 (96mer) (SEQ.ID.NO:138) 5' GCT TGT TGT TGC CGG TGG CGG  
TGG CGG CGC CCA GCA GAG GGT TCA CGG GCC CGC AGT GCT GCT TCT  
CGG CCA GGC CGC AGT GGC CAG GGC GAG TGG 3'

18M 829-925 (97mer) (SEQ.ID.NO:139) 5' GCC ACC GCC ACC GGC AAC AAC  
AAG CGC CGC AAG CTG TGC AGC GGC AAC ACC ACT CCC ATC ATC CAC  
CTG AAG GGC GAC CGC AAC AGC CTG AAG TGC C 3'

18N 900-996 (97mer) (SEQ.ID.NO:140) 5' GGC GCC GGT CCA GTG CCA GGT  
GCT GCT GAT GTC GCG GTA GTG GTC GCT GTG CTT GCG CAG GCG GTA  
CCG CAG GCA CTT CAG GCT GTT GCG GTC GCC C 3'

18O 974-1072 (99mer) (SEQ.ID.NO:141) 5' GCA CCT GGC ACT GGA CCG GCG  
CCG GGA ACG AGA AGA CCG GCA TCC TGA CCG TGA CCT ACC ACA GCG  
AGA CCC AGC GCA CCA AGT TCC TGA ACA CCG TGG 3'

18P 1048-1145 (98mer) (SEQ.ID.NO:142) 5' CTC GAG AGA TCT CCC GGG TCT  
AGA GCT TAC ATG GTC ATG TAG CCC ACC AGG ATC TGC ACG CTG TCG  
GGG ATG GCC ACG GTG TTC AGG AAC TTG GTG CG 3'

18PA 25mer (SEQ.ID.NO:143) 5' GAA TTC AGA TCT GAT ATC ACC ATG C 3'

18PD 23mer (SEQ.ID.NO:144) 5' CCT CGG TCT TGT AGG CGC TCT GG 3'

18PE 21mer (SEQ.ID.NO:145) 5' CCC AGA GCG CCT ACA AGA CCG 3'

18PH 21mer (SEQ.ID.NO:146) 5' CCG TAC TTC TCG CAC TCG CTC 3'

18PI 20mer (SEQ.ID.NO:147) 5' CGA GTT CAA GAG CGA GTG CG 3'

18PL 21mer (SEQ.ID.NO:148) 5' GCT TGT TGT TGC CGG TGG CGG 3'

18PM 25mer (SEQ.ID.NO:149) 5' GCC ACC GCC ACC GGC AAC AAC AAG C 3'

18PP 26mer (SEQ.ID.NO:150) 5' CTC GAG AGA TCT CCC GGG TCT AGA GC 3'



FIGURE 25

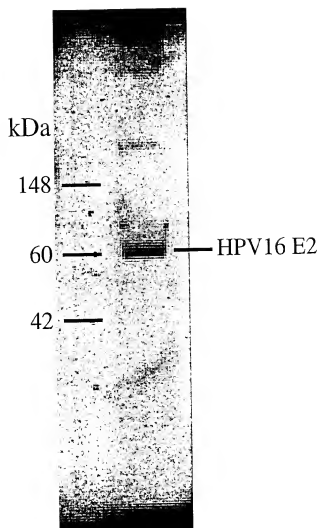


FIGURE 26

